

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/856,681

DATE: 09/13/2001  
TIME: 17:40:26

Input Set : A:\Sequence.txt  
Output Set: N:\CRF3\09132001\I856681.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Behl, Christian  
4 Klostermann, Andreas  
6 <120> TITLE OF INVENTION: Human semaphorin 6A-1 (SEMA6A-A), a gene involved  
7 in neuronal development and regeneration mechanisms  
8 during apoptosis, and its use as a potential drug target  
10 <130> FILE REFERENCE: 48498-258443  
12 <140> CURRENT APPLICATION NUMBER: 09/856,681  
13 <141> CURRENT FILING DATE: 2001-05-22  
15 <150> PRIOR APPLICATION NUMBER: PCT/EP99/09215  
16 <151> PRIOR FILING DATE: 1999-11-26  
18 <150> PRIOR APPLICATION NUMBER: 98122441.3  
19 <151> PRIOR FILING DATE: 1998-11-26  
21 <160> NUMBER OF SEQ ID NOS: 7  
23 <170> SOFTWARE: PatentIn Ver. 2.1

run

#### ERRORED SEQUENCES

299 <210> SEQ ID NO: 2  
300 <211> LENGTH: 1030  
301 <212> TYPE: PRT  
302 <213> ORGANISM: Homo sapiens  
304 <400> SEQUENCE: 2  
305 Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala  
306 1 5 10 15  
308 Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly  
309 20 25 30  
311 Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg  
312 35 40 45  
314 Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met  
315 50 55 60  
317 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp  
318 65 70 75 80  
320 Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr  
321 85 90 95  
323 Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys  
324 100 105 110  
326 His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn  
327 115 120 125  
329 Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys  
330 130 135 140  
332 Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser  
333 145 150 155 160  
335 Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu  
336 165 170 175  
338 Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala  
339 180 185 190

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341 Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
342      195      200      205
344 Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
345      210      215      220
347 Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Phe Arg Glu Ile Ala
348 225      230      235      240
350 Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
351      245      250      255
353 Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
354      260      265      270
356 Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
357      275      280      285
359 Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
360      290      295      300
362 Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
363 305      310      315      320
365 Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
366      325      330      335
368 Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
369      340      345      350
371 Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
372      355      360      365
374 Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
375      370      375      380
377 Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
378 385      390      395      400
380 Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
381      405      410      415
383 Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
384      420      425      430
386 Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
387      435      440      445
389 Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
390      450      455      460
392 Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
393 465      470      475      480
395 Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
396      485      490      495
398 Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
399      500      505      510
401 Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
402      515      520      525
404 Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
405      530      535      540
407 Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
408 545      550      555      560
410 Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
411      565      570      575
413 Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr

```

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414		580		585		590
416	Ala	Gln	Glu	Gly	Tyr	Glu
417		595		600		605
419	Leu	Leu	Asp	Ser	Pro	Asp
420		610		615		620
422	His	Asn	His	Gln	Asp	Lys
423	625			630		635
425	Gly	His	Asp	Gln	Leu	Val
426		645		650		655
428	Leu	Ala	Phe	Val	Met	Gly
429		660		665		670
431	Val	Cys	Asp	His	Arg	Arg
432		675		680		685
434	Lys	Glu	Leu	Thr	His	Ser
435		690		695		700
437	Leu	Ser	Gly	Leu	Phe	Gly
438	705			710		715
440	Ala	Ile	Leu	Thr	Pro	Leu
441		725		730		735
443	Asn	Thr	Ala	Lys	Met	Leu
444		740		745		750
446	Thr	Ala	Leu	Pro	Thr	Pro
447		755		760		765
449	Lys	Pro	Ser	Arg	Gly	Ser
450		770		775		780
452	Asn	Ala	Cys	Thr	Lys	Asp
453	785			790		795
455	Thr	Asp	Leu	Pro	Leu	Arg
456		805		810		815
458	Val	Leu	Pro	Ile	Thr	Gln
459		820		825		830
461	Pro	Lys	Met	Ser	Glu	Val
462		835		840		845
464	Thr	Leu	Glu	Tyr	Lys	Thr
465		850		855		860
467	Asn	His	Gly	Val	Asn	Leu
468	865			870		875
471	Val	Pro	Gln	Arg	Glu	Ala
472		885		890		895
474	Gln	Thr	Gly	Leu	Ser	Lys
475		900		905		910
477	Gly	Val	Asp	Tyr	Lys	Arg
478		915		920		925
480	His	Gln	Ala	Thr	Thr	Leu
481		930		935		940
483	Ser	His	Leu	Ser	Arg	Asn
484	945			950		955
486	Pro	Ala	Pro	Gln	Arg	Val
487		965		970		975

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489 Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
490                               980 985 990
492 Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
493                               995 1000 1005
495 Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
496 1010 1015 1020
498 Pro Asn Asp Ala Cys Thr
E--> 499 025/026 1030
880 <210> SEQ ID NO: 7
881 <211> LENGTH: 1030
882 <212> TYPE: PRT
883 <213> ORGANISM: Homo sapiens
885 <400> SEQUENCE: 7
886 Met Arg Ser Glu Ala Leu Leu Leu Tyr Phe Thr Leu Leu His Phe Ala
887 1 5 10 15
889 Gly Ala Gly Phe Pro Glu Asp Ser Glu Pro Ile Ser Ile Ser His Gly
890 20 25 30
892 Asn Tyr Thr Lys Gln Tyr Pro Val Phe Val Gly His Lys Pro Gly Arg
893 35 40 45
895 Asn Thr Thr Gln Arg His Arg Leu Asp Ile Gln Met Ile Met Ile Met
896 50 55 60
898 Asn Gly Thr Leu Tyr Ile Ala Ala Arg Asp His Ile Tyr Thr Val Asp
899 65 70 75 80
901 Ile Asp Thr Ser His Thr Glu Glu Ile Tyr Cys Ser Lys Lys Leu Thr
902 85 90 95
904 Trp Lys Ser Arg Gln Ala Asp Val Asp Thr Cys Arg Met Lys Gly Lys
905 100 105 110
907 His Lys Asp Glu Cys His Asn Phe Ile Lys Val Leu Leu Lys Lys Asn
908 115 120 125
910 Asp Asp Ala Leu Phe Val Cys Gly Thr Asn Ala Phe Asn Pro Ser Cys
911 130 135 140
913 Arg Asn Tyr Lys Met Asp Thr Leu Glu Pro Phe Gly Asp Glu Phe Ser
914 145 150 155 160
916 Gly Met Ala Arg Cys Pro Tyr Asp Ala Lys His Ala Asn Val Ala Leu
917 165 170 175
919 Phe Ala Asp Gly Lys Leu Tyr Ser Ala Thr Val Thr Asp Phe Leu Ala
920 180 185 190
922 Ile Asp Ala Val Ile Tyr Arg Ser Leu Gly Glu Ser Pro Thr Leu Arg
923 195 200 205
925 Thr Val Lys His Asp Ser Lys Trp Leu Lys Glu Pro Tyr Phe Val Gln
926 210 215 220
928 Ala Val Asp Tyr Gly Asp Tyr Ile Tyr Phe Phe Arg Glu Ile Ala
929 225 230 235 240
931 Val Glu Tyr Asn Thr Met Gly Lys Val Val Phe Pro Arg Val Ala Gln
932 245 250 255
934 Val Cys Lys Asn Asp Met Gly Gly Ser Gln Arg Val Leu Glu Lys Gln
935 260 265 270
937 Trp Thr Ser Phe Leu Lys Ala Arg Leu Asn Cys Ser Val Pro Gly Asp
938 275 280 285

```

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```

941 Ser His Phe Tyr Phe Asn Ile Leu Gln Ala Val Thr Asp Val Ile Arg
942      290      295      300
944 Ile Asn Gly Arg Asp Val Val Leu Ala Thr Phe Ser Thr Pro Tyr Asn
945 305      310      315      320
947 Ser Ile Pro Gly Ser Ala Val Cys Ala Tyr Asp Met Leu Asp Ile Ala
948      325      330      335
950 Ser Val Phe Thr Gly Arg Phe Lys Glu Gln Lys Ser Pro Asp Ser Thr
951      340      345      350
953 Trp Thr Pro Val Pro Asp Glu Arg Val Pro Lys Pro Arg Pro Gly Cys
954      355      360      365
956 Cys Ala Gly Ser Ser Ser Leu Glu Arg Tyr Ala Thr Ser Asn Glu Phe
957      370      375      380
959 Pro Asp Asp Thr Leu Asn Phe Ile Lys Thr His Pro Leu Met Asp Glu
960 385      390      395      400
962 Ala Val Pro Ser Ile Phe Asn Arg Pro Trp Phe Leu Arg Thr Met Val
963      405      410      415
965 Arg Tyr Arg Leu Thr Lys Ile Ala Val Asp Thr Ala Ala Gly Pro Tyr
966      420      425      430
968 Gln Asn His Thr Val Val Phe Leu Gly Ser Glu Lys Gly Ile Ile Leu
969      435      440      445
971 Lys Phe Leu Ala Arg Ile Gly Asn Ser Gly Phe Leu Asn Asp Ser Leu
972      450      455      460
974 Phe Leu Glu Glu Met Ser Val Tyr Asn Ser Glu Lys Cys Ser Tyr Asp
975 465      470      475      480
977 Gly Val Glu Asp Lys Arg Ile Met Gly Met Gln Leu Asp Arg Ala Ser
978      485      490      495
980 Ser Ser Leu Tyr Val Ala Phe Ser Thr Cys Val Ile Lys Val Pro Leu
981      500      505      510
983 Gly Arg Cys Glu Arg His Gly Lys Cys Lys Lys Thr Cys Ile Ala Ser
984      515      520      525
986 Arg Asp Pro Tyr Cys Gly Trp Ile Lys Glu Gly Gly Ala Cys Ser His
987      530      535      540
989 Leu Ser Pro Asn Ser Arg Leu Thr Phe Glu Gln Asp Ile Glu Arg Gly
990 545      550      555      560
992 Asn Thr Asp Gly Leu Gly Asp Cys His Asn Ser Phe Val Ala Leu Asn
993      565      570      575
995 Gly His Ser Ser Ser Leu Leu Pro Ser Thr Thr Thr Ser Asp Ser Thr
996      580      585      590
998 Ala Gln Glu Gly Tyr Glu Ser Arg Gly Gly Met Leu Asp Trp Lys His
999      595      600      605
1001 Leu Leu Asp Ser Pro Asp Ser Thr Asp Pro Leu Gly Ala Val Ser Ser
1002      610      615      620
1004 His Asn His Gln Asp Lys Lys Gly Val Ile Arg Glu Ser Tyr Leu Lys
1005 625      630      635      640
1007 Gly His Asp Gln Leu Val Pro Val Thr Leu Leu Ala Ile Ala Val Ile
1008      645      650      655
1010 Leu Ala Phe Val Met Gly Ala Val Phe Ser Gly Ile Thr Val Tyr Cys
1011      660      665      670
1013 Val Cys Asp His Arg Arg Lys Asp Val Ala Val Val Gln Arg Lys Glu

```

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```

1014          675          680          685
1016 Lys Glu Leu Thr His Ser Arg Arg Gly Ser Met Ser Ser Val Thr Lys
1017          690          695          700
1019 Leu Ser Gly Leu Phe Gly Asp Thr Gln Ser Lys Asp Pro Lys Pro Glu
1020 705          710          715          720
1022 Ala Ile Leu Thr Pro Leu Met His Asn Gly Lys Leu Ala Thr Pro Gly
1023          725          730          735
1025 Asn Thr Ala Lys Met Leu Ile Lys Ala Asp Gln His His Leu Asp Leu
1026          740          745          750
1028 Thr Ala Leu Pro Thr Pro Glu Ser Thr Pro Thr Leu Gln Gln Lys Arg
1029          755          760          765
1031 Lys Pro Ser Arg Gly Ser Arg Glu Trp Glu Arg Asn Gln Asn Leu Ile
1032          770          775          780
1034 Asn Ala Cys Thr Lys Asp Met Pro Pro Met Gly Ser Pro Val Ile Pro
1035 785          790          795          800
1037 Thr Asp Leu Pro Leu Arg Ala Ser Pro Ser His Ile Pro Ser Val Val
1038          805          810          815
1040 Val Leu Pro Ile Thr Gln Gln Gly Tyr Gln His Glu Tyr Val Asp Gln
1041          820          825          830
1043 Pro Lys Met Ser Glu Val Ala Gln Met Ala Leu Glu Asp Gln Ala Ala
1044          835          840          845
1046 Thr Leu Glu Tyr Lys Thr Ile Lys Glu His Leu Ser Ser Lys Ser Pro
1047          850          855          860
1049 Asn His Gly Val Asn Leu Val Glu Asn Leu Asp Ser Leu Pro Pro Lys
1050 865          870          875          880
1052 Val Pro Gln Arg Glu Ala Ser Leu Gly Pro Pro Gly Ala Ser Leu Ser
1053          885          890          895
1055 Gln Thr Gly Leu Ser Lys Arg Leu Glu Met His His Ser Ser Tyr
1056          900          905          910
1059 Gly Val Asp Tyr Lys Arg Ser Tyr Pro Thr Asn Ser Leu Thr Arg Ser
1060          915          920          925
1062 His Gln Ala Thr Thr Leu Lys Arg Asn Asn Thr Asn Ser Ser Asn Ser
1063          930          935          940
1065 Ser His Leu Ser Arg Asn Gln Ser Phe Gly Arg Gly Asp Asn Pro Pro
1066 945          950          955          960
1068 Pro Ala Pro Gln Arg Val Asp Ser Ile Gln Val His Ser Ser Gln Pro
1069          965          970          975
1071 Ser Gly Gln Ala Val Thr Val Ser Arg Gln Pro Ser Leu Asn Ala Tyr
1072          980          985          990
1074 Asn Ser Leu Thr Arg Ser Gly Leu Lys Arg Thr Pro Ser Leu Lys Pro
1075          995          1000          1005
1077 Asp Val Pro Pro Lys Pro Ser Phe Ala Pro Leu Ser Thr Ser Met Lys
1078          1010          1015          1020
1080 Pro Asn Asp Ala Cys Thr
E--> 1081 (025)          1030
      1025

```

VERIFICATION SUMMARY

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Input Set : A:\Sequence.txt

Output Set: N:\CRF3\09132001\I856681.raw

L:499 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
L:1081 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:7